



IFWO

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/538,038A

DATE: 06/20/2006  
TIME: 15:28:31

Input Set : A:\Sequence Listing.TXT  
Output Set: N:\CRF4\06202006\J538038A.raw

2 <110> APPLICANT: Givaudan SA  
W--> 3 <120> TITLE OF INVENTION: G-Proteins  
W--> 4 <130> FILE REFERENCE: 30069PCT  
W--> 5 <140> CURRENT APPLICATION NUMBER: US 10/538,038A  
C--> 6 <141> CURRENT FILING DATE: 2005-06-08  
7 <150> PRIOR APPLICATION NUMBER: US 60/434,790  
8 <151> PRIOR FILING DATE: 2002-12-18  
W--> 9 <160> NUMBER OF SEQ ID: 2

## ERRORED SEQUENCES

W--> 10 <210> SEQ ID NO: 1  
11 <211> LENGTH: 1122 <212> DNA  
12 <213> ORGANISM: Homo sapiens  
W--> 13 <220> FEATURE:  
14 <221> NAME/KEY: CDS  
15 <222> LOCATION: (1)...(1122)  
16 <223> OTHER INFORMATION:  
E--> 17 <212> TYPE: ignore this  
W--> 17 <400> SEQUENCE: 1  
18 atggccgcgt cgctgacctg ggcgtgtgc ccctggtgc tgacggagga tgagaaggcc 60  
19 gcccggggg tggaccagga gatcaacagg atccctttgg agcagaagaa gcaggaccgc 120  
20 ggggagctga agctgtgtgtc tttggggcca ggccggagcg ggaagagcac cttcatcaag 180  
21 cagatgcggta tcataccacgg cgccggctac tggaggagg agcgcacagg ctccggccc 240  
22 ctggcttacc agaacatctt cgtgtccatg cggccatga tggaggccat ggagcggctg 300  
23 cagattccat tcaagcaggcc cgagagcaag caccacgcta gcctggtcat gagccaggac 360  
24 ccctataaag tgaccacgtt tgagaagcgc taegctgcgg ccatgcagt gctgtggagg 420  
25 gatgcggca tccggggctcg ctatgagcgt cggcgggaat tccacctgt cgattcagcc 480  
26 gtgtactacc tgccccacat ggagcgcate accaggagg gctacgtccc cacagcttag 540  
27 gacgtgtccgc gcaagccgcat gcccacact ggcatcaaag agtactgtt ctccgtgcag 600  
28 aaaaccaacc tggggatgtt ggacgtgggg ggcagaagt cagagcgtaa gaaatggatc 660  
29 cattgtttcg agaacgtgtat cgccctcata tacctggct cactgagtgta atacgaccag 720  
30 tgcctggagg agaacaaacca ggagaaccgc atgaaggaga gcctgcatt gtttggact 780  
31 atccctggaaac taccctggtt caaaaagcaca tccgtcatcc tctttctcaa caaaaccgac 840  
32 atccctggagg agaaaaatccc cacctcccac ctggctacat atttccccag tttccagggc 900  
33 cctaagcagg atgtgaggc agccaagagg ttcatctgg acatgtacac gaggatgtac 960  
34 accgggtgcg tgacggccc cgaggcgcg aactaaaaaa aagaagataa gggaaatctat 1020  
35 tctcacatga cctgcgtac tgacacacaa aacgtaaat tgcgtttga tgccgtgaca 1080  
36 gatataataa taaaagagaa cctcaaaagac tggggctct tc 1122

*Does Not Comply  
Corrected Diskette Needed*

*all  
pr 1-3*

*insert a hard return*

? (see p.3 - the last-numbered anno and states "395")

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41 <213> ORGANISM: Homo sapiens  
 W--> 42 <400> SEQUENCE: 2  
 43 Met Ala Arg Ser Leu Thr Trp Arg Cys Cys Pro Trp Cys Leu Thr Glu 1  
 E--> 44 5 10 15 10 15  
 46 Asp Glu Lys Ala Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu  
 E--> 47 20 20 25 30 30  
 49 Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu  
 E--> 50 35 40 45  
 52 Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile  
 E--> 53 50 55 60  
 55 Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro  
 E--> 56 65 70 75 80  
 58 Leu Val Tyr Glu Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala  
 E--> 59 85 90 95  
 61 Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His  
 E--> 62 100 105 110  
 64 Ala Ser Leu Val Met Ser Gln Asp PRO Tyr Lys Val Thr Thr Phe Glu  
 E--> 65 115 120 125  
 67 Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile  
 E--> 68 130 135 140  
 70 Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala  
 E--> 71 145 150 155 160  
 74 Val Tyr Tyr Ieu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val  
 E--> 75 165 170 175  
 77 Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile  
 E--> 78 180 185 190  
 80 Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp  
 E--> 81 195 200 205  
 83 Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu  
 E--> 84 210 215 220  
 86 Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Glu  
 E--> 87 225 230 235 240  
 89 Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Ieu Ala  
 E--> 90 245 250 255  
 92 Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val  
 E--> 93 260 265 270  
 95 Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr  
 E--> 96 275 280 285  
 E--> 98 Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp  
 E--> 99 290 295 300  
 101 Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr  
 E--> 102 305 310 315 320  
 104 Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Asn Leu Lys Lys Glu Asp  
 E--> 105 325 330 335  
 107 Lys Glu Ile Tyr Ser His Met Thr Cys Ala Thr Asp Thr Gln Asn Val  
 E--> 108 340 345 350  
 110 Lys Phe Val Phe Asp Ala Val Thr Asp Ile Ile Lys Glu Asn Leu  
 E--> 111 355 360 365  
 113 Lys Asp Cys Gly Leu Phe Ser His Leu Ala Thr Tyr Phe Pro Ser

*of delete*

*misaligned*

*amino acid  
numbers*

*(see item 3  
on Error  
summary*

*sheet)*

*invalid amino acid designator*

*Q1n*

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E--> 114 370  
E--> 116 Phe Gln Gly Pro Lys Gin Asp  
E--> 117 385 390

375  
380

invalid amino acid designator

Gly

## VERIFICATION SUMMARY

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Input Set : A:\Sequence Listing.TXT

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L:3 M:283 W: Missing Blank Line separator, <120> field identifier  
L:4 M:283 W: Missing Blank Line separator, <130> field identifier  
L:5 M:283 W: Missing Blank Line separator, <140> field identifier  
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:9 M:283 W: Missing Blank Line separator, <160> field identifier  
L:10 M:283 W: Missing Blank Line separator, <210> field identifier  
L:13 M:283 W: Missing Blank Line separator, <220> field identifier  
L:17 M:282 E: Numeric Field Identifier Missing, <212> is required.  
L:17 M:283 W: Missing Blank Line separator, <400> field identifier  
L:17 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:16  
L:42 M:283 W: Missing Blank Line separator, <400> field identifier  
L:44 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
M:332 Repeated in SeqNo=2  
L:98 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
L:116 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1